SEQUENCE LISTING

<110> Sturmer, Rainer
      Kesseler, Maria
      Hauer, Bernhard
      Friedrich, Thomas
      Breuer, Michael

<120> Methods for the production of
      3-methylamino-1-(thiene-2-yl)-propane-1-ol

<130> 13111-00035-US

<140> US/10/573,130
<141> 2006-03-23

<150> PCT/EP2004/010939
<151> 2004-09-30

<150> DE 103 45 772.0
<151> 2003-10-01

<160> 44

<170> PatentIn version 3.3


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<213> Lactobacillus brevis

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Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
1               5                   10                  15
Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
            20                  25                  30
Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala
        35                  40                  45


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Ser Asn Ala Leu Val Thr Gly Gly Ser Arg Val Ile Gly Ala Gly Gly
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Phe Ile


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Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr
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ttg ggt atc ggt tta gct atc gcc acg aag ttc gtt gaa gaa ggg gct      96
Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
                20                  25                  30
aag gtc atg att acc ggc cgg cac agc gat gtt ggt gaa aaa gca gct     144
Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
            35                  40                  45
aag agt gtc ggc act cct gat cag att caa ttt ttc caa cat gat tct     192
Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
        50                  55                  60
tcc gat gaa gac ggc tgg acg aaa tta ttc gat gca acg gaa aaa gcc     240
Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
65                  70                  75                  80
ttt ggc cca gtt tct aca tta gtt aat aac gct ggg atc gcg gtt aac     288
Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
                85                  90                  95
aag agt gtc gaa gaa acc acg act gct gaa tgg cgt aaa cta tta gcc     336
Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
                100                 105                 110
gtc aac ctt gat ggt gtc ttc ttc ggt acc cga tta ggg att caa cgg     384
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
            115                 120                 125
atg aag aac aaa ggc tta ggg gct tcc atc atc aac atg tct tcg atc     432
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
        130                 135                 140
gaa ggc ttt gtg ggt gat cct agc tta ggg gct tac aac gca tct aaa     480
Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
145                 150                 155                 160
ggg gcc gta cgg att atg tcc aag tca gct gcc tta gat tgt gcc cta     528
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
                165                 170                 175
aag gac tac gat gtt cgg gta aac act gtt cac cct ggc tac atc aag     576
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
                180                 185                 190
aca cca ttg gtt gat gac cta cca ggg gcc gaa gaa gcg atg tca caa     624
Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
            195                 200                 205
cgg acc aag acg cca atg ggc cat atc ggt gaa cct aac gat att gcc     672
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
        210                 215                 220
tac atc tgt gtt tac ttg gct tct aac gaa tct aaa ttt gca acg ggt     720
Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
225                 230                 235                 240
tct gaa ttt gta gtt gac ggt ggc tac act gct caa                     756
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                20                  25                  30
Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
            35                  40                  45
Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
        50                  55                  60
Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
65                  70                  75                  80
Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
                85                  90                  95
Lys Ser Val Glu Glu Thr Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
            100                 105                 110
Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
        115                 120                 125
Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
    130                 135                 140
Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
145                 150                 155                 160
Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
                165                 170                 175
Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
            180                 185                 190
Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
        195                 200                 205
Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
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Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
225                 230                 235                 240
Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
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1               5                   10                  15
att aag ctc gcc gag gag ggc tac agc gtc acg att gcg tct cgc ggc      96
Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly
                20                  25                  30
ctt aag cag ctc gag gct gtg aag gcc aaa cta ccc att gtg aag cag     144

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Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln
        35                  40                  45
gga cag gtt cac cac gtg tgg cag ctt gat ctc agt gat gtc gac gct        192
Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala
        50                  55                  60
gcg gcc gcc ttc aaa ggg tcg ccg cta cct gcc agc cgc tac gac gtg        240
Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val
65                  70                  75                  80
ctc gtc agc aat gct ggc gtg gcc cag ttt agc ccg ttc atc gag cat        288
Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His
                    85                  90                  95
gcg aag cag gac tgg tcg cag atg ctt gcc atc aat ctg gcg gca ccc        336
Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro
                100                 105                 110
att gcg ctg gcc cag aca ttt gct aag gcc att ggc gac aag ccg cgc        384
Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg
        115                 120                 125
aac aca ccg gcc cac att gtg ttt gtc tcg tcg aac gtc tcg ttg cga        432
Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg
        130                 135                 140
ggc ttc ccg aac atc ggc gtc aac tcc atc acc ccc ggc a                  472
Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly
145                 150                 155


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            20                  25                  30
Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln
        35                  40                  45
Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala
        50                  55                  60
Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val
65                  70                  75                  80
Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His
                    85                  90                  95
Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro
                100                 105                 110
Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg
        115                 120                 125
Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg
        130                 135                 140
Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly
145                 150                 155


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gccggggttg atsswgttsa cgccgat                                    27

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Ser Thr Thr Ser Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly
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Ala Ala



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Ile Gly Val Asn Ser Ile Asn Pro Gly
1               5


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Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr Leu
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Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala Lys
            20                  25                  30
Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Xaa Xaa
            35                  40                  45
Ser Val Gly Thr Xaa Asp Gln Ile Gln Phe Xaa Xaa
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Arg Arg Xaa Xaa
            20


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Asp Glu Asp Gly
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Xaa Xaa Xaa Xaa
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1               5


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1               5                   10                  15


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Xaa Xaa



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1               5                   10                  15
Xaa
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Xaa Xaa Xaa Xaa
            20


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1               5


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<400>  27

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15


<210>  28
<211>  20
<212>  PRT
<213>  Lactobacillus brevis

<220>
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<220>
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<223> Xaa is Ile (main residue from sequencing), Val, or Leu
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<220>
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<400>  28

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15
Xaa Xaa Xaa Xaa
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<210>  29
<211>  25
<212>  PRT
<213>  Lactobacillus brevis
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<220>
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<223>  Xaa is Pro or Arg

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<223>  Xaa is His or Tyr

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<220>
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<223>  Xaa is Phe or Thr

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<220>
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<220>
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<222>  (25)..(25)

<400>  29

Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa
1               5                   10                  15
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Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Gln
            20                  25
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<210>  30
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<213>  Lactobacillus brevis

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<220>
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<220>
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<223>  Xaa is unknown, Ile, or Asp

<220>
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<222>  (11)..(20)
<223>  Xaa is unknown

<400>  30
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Xaa Xaa Lys Leu Xaa Ala Val Asn Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15
Xaa Xaa Xaa Xaa
            20
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<210>  31
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<213>  Lactobacillus brevis

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<223>  Xaa is Phe (main residue from sequencing) or Val
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<220>
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<220>
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<223> Xaa is Lys (main residue from sequencing) or His

<220>
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<222> (8)..(8)
<223> Xaa is Gln (main residue from sequencing) or Pro

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<223> Xaa is Asn (main residue from sequencing), Lys, or Asp

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<220>
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<220>
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<223>  Xaa is Val (main residue from sequencing) or Asp


<220>
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<223>  Xaa is Arg (main residue from sequencing), Asp, or Leu


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<222>  (20)..(20)


<400>  31

Xaa Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15
Xaa Xaa Xaa Pro
            20



<210>  32
<211>  30
<212>  PRT
<213>  Lactobacillus brevis


<220>
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<223>  Xaa is Val (main residue from sequencing) or Leu


<220>
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<223>    Xaa is Pro (main residue from sequencing), Gln, or Tyr


<220>
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<223>    Xaa is Ser (main residue from sequencing), Asn, Arg, or Lys


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<223>    Xaa is Leu (main residue from sequencing), Met, or Ala


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<223>    Xaa is Gly (main residue from sequencing) or Lys


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<223>    Xaa is Tyr (main residue from sequencing), Gly, or Lys


<220>
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<223>    Xaa is Asn (main residue from sequencing), Gly, or Ala


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<223>    Xaa is Gly (main residue from sequencing), Met, or Ser
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<220>
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<222> (29)..(30)
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<400> 32

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1               5                   10                  15
Xaa Xaa Xaa Xaa Met Ser Lys Ser Ala Ala Leu Asp Xaa Xaa
            20                  25                  30


<210> 33
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<212> PRT
<213> Lactobacillus brevis

<220>
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<222> (5)..(10)
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<400> 33

Phe Val Val Asp Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10


<210> 34
<211> 20
<212> PRT
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<213>  Lactobacillus brevis

<220>
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<220>
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<223>  Xaa is  Lys (main residue from sequencing), Asp, or Pro

<220>
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<220>
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<222>  (12)..(12)

<220>
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<400>  34

Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Thr Glu Glu Xaa Xaa Xaa Xaa
1                   5                   10                  15
Xaa Xaa Xaa Xaa
            20
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<210>  35
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<212>  PRT
<213>  Lactobacillus brevis

<220>
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<400>  35

Phe Val Val Asp Gly Gly Tyr Thr Ala Gln Xaa Xaa Xaa Xaa
1               5                   10


<210>  36
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<213>  Lactobacillus brevis

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<220>
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<400>  36

Xaa Xaa Leu Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly
1               5                   10                  15
Tyr Ile Lys Thr Pro Leu Val Xaa Asp Leu Pro Gly Ala Xaa
            20                  25                  30


<210>  37
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<212>  PRT
<213>  Lactobacillus brevis

<400>  37
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Lys Ala Ala Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe
1               5                   10                  15


<210> 38
<211> 13
<212> PRT
<213> Lactobacillus brevis

<400> 38

Gly Ala Lys Val Met Ile Thr Gly Arg His Ser Asp Val
1               5                   10


<210> 39
<211> 10
<212> PRT
<213> Lactobacillus brevis

<220>
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<220>
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<223> Xaa is Thr (main residue from sequencing), Phe, or Ile

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<223> Xaa is Ser (main residue from sequencing) or Tyr

<220>
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<222> (8)..(8)
<223> Xaa is Glu (main residue from sequencing) or Leu

<400> 39

Xaa Lys Xaa Ala Xaa Xaa Xaa Xaa Phe Val
1               5                   10

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<210>  40
<211>  25
<212>  PRT
<213>  Lactobacillus brevis

<220>
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<223>  Xaa is Arg (main residue from sequencing), Lys, or Gly

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<220>
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<223>  Xaa is Lys (main residue from sequencing) or Gly

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<220>
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<223>  Xaa is Asp (main residue from sequencing) or Asn

<220>
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<223>  Xaa is Asp (main residue from sequencing) or Met

<220>
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<222>  (22)..(22)
<223>  Xaa is Pro (main residue from sequencing) or Leu

<400>  40
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Xaa Xaa Xaa Xaa Xaa Asn Thr Val His Pro Gly Tyr Ile Xaa Xaa Pro
1               5                   10                  15
Leu Val Xaa Xaa Leu Xaa Gly Ala Glu
            20              25
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<210>   41
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<213>   Lactobacillus brevis

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<220>
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<222>   (39)..(40)
<223>   Xaa is unknown

<400>   41
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Trp Xaa Lys Leu Leu Ala Val Asn Leu Asp Gly Val Phe Phe Gly Thr
1               5                   10                  15
Arg Leu Gly Ile Gln Arg Met Lys Asn Lys Gly Leu Gly Ala Ser Ile
            20                  25                  30
Ile Asn Met Ser Ser Ile Xaa Xaa
            35              40
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<210>   42
<211>   40
<212>   PRT
<213>   Lactobacillus brevis

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<222>   (3)..(3)
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<221>   misc_feature
<222>   (4)..(4)
<223>   Xaa is Gln (main residue from sequencing), Leu, Lys, or Glu

<220>
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<222>   (5)..(5)
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<223>  Xaa is Arg (main residue from sequencing), Leu, or Ser

<220>
<221>  misc_feature
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<223>  Xaa is Thr (main residue from sequencing), Ala, or Val

<220>
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<222>  (7)..(7)
<223>  Xaa is Lys (main residue from sequencing), Val, or Gly

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<222>  (8)..(8)
<223>  Xaa is Thr (main residue from sequencing) or Asn

<220>
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<223>  Xaa is Pro (main residue from sequencing) or Leu

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<223>  Xaa is Met (main residue from sequencing), Asp, or Ala

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<223>  Xaa is Gly (main residue from sequencing), Gln, or Tyr

<220>
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<222>  (12)..(12)
<223>  Xaa is His (main residue from sequencing), Val, Ile, or Asn

<220>
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<223>  Xaa is Ile (main residue from sequencing), Phe, Ala, or Gln

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<220>
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<220>
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<400>   42

Ala Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15
Xaa Xaa Xaa Xaa Xaa Arg Met Lys Xaa Lys Xaa Leu Gly Ala Ser Ile
            20                  25                  30
Ile Asn Met Ser Xaa Xaa Xaa Gly
        35                  40


<210>   43
<211>   15
<212>   PRT
<213>   Lactobacillus brevis

<220>
<221> misc_feature
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<400>   43

Ser Lys Phe Ala Thr Gly Ser Glu Phe Val Val Xaa Xaa Xaa Xaa
1               5                   10                  15


<210>   44
<211>   15
<212>   PRT
<213>   Lactobacillus brevis

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<220>
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<223>   Xaa is Thr (main residue from sequencing), Ile, or Pro

<220>
<221>   misc_feature
<222>   (6)..(6)
<223>   Xaa is Gly (main residue from sequencing), Leu, or Asp

<220>
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<222>   (7)..(7)
<223>   Xaa is Ser (main residue from sequencing) or Gln

<220>
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<220>
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<220>
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<222>   (12)..(12)
```

<223>   Xaa is Asp (main residue from sequencing), Gln, or Lys

<220>
<221>  misc_feature
<222>  (13)..(15)
<223>  Xaa is unknown

<400>  44

Xaa Lys Phe Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15